

SEQUENCE LISTING

<110> Goodman, Corey
Kid, Thomas
Brose, Katja
Tessier-Lavigne, Marc

<120> Modulating Robo: Ligand Interactions

<130> B98-031-3

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<150> 60/065,544

<151> 1997-11-14

<150> 60/081,057

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<170> PatentIn Ver. 2.0

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 Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg
 340 345 350
 Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
 355 360 365
 Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn
 370 375 380
 Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His
 385 390 395 400
 Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
 405 410 415
 Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
 420 425 430
 Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
 435 440 445
 Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
 450 455 460
 Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
 465 470 475 480
 Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
 485 490 495
 Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
 500 505 510

09922600.080304

Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Asn	Lys	Ile	Pro	Glu	His	Ile	Pro
		515					520					525			
Gln	Tyr	Thr	Ala	Glu	Leu	Arg	Leu	Asn	Asn	Asn	Glu	Phe	Thr	Val	Leu
	530					535					540				
Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys	Leu	Pro	Gln	Leu	Arg	Lys	Ile	Asn
545					550					555					560
Phe	Ser	Asn	Asn	Lys	Ile	Thr	Asp	Ile	Glu	Gly	Ala	Phe	Glu	Gly	
				565					570				575		
Ala	Ser	Gly	Val	Asn	Glu	Ile	Leu	Leu	Thr	Ser	Asn	Arg	Leu	Glu	Asn
			580					585					590		
Val	Gln	His	Lys	Met	Phe	Lys	Gly	Leu	Glu	Ser	Leu	Lys	Thr	Leu	Met
		595					600					605			
Leu	Arg	Ser	Asn	Arg	Ile	Thr	Cys	Val	Gly	Asn	Asp	Ser	Phe	Ile	Gly
610					615						620				
Leu	Ser	Ser	Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Gln	Ile	Thr	Thr
625					630					635					640
Val	Ala	Pro	Gly	Ala	Phe	Asp	Thr	Leu	His	Ser	Leu	Ser	Thr	Leu	Asn
				645					650					655	
Leu	Leu	Ala	Asn	Pro	Phe	Asn	Cys	Asn	Cys	Tyr	Leu	Ala	Trp	Leu	Gly
			660					665					670		
Glu	Trp	Leu	Arg	Lys	Lys	Arg	Ile	Val	Thr	Gly	Asn	Pro	Arg	Cys	Gln
		675					680					685			
Lys	Pro	Tyr	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala	Ile	Gln
	690					695					700				
Asp	Phe	Thr	Cys	Asp	Asp	Gly	Asn	Asp	Asp	Asn	Ser	Cys	Ser	Pro	Leu
705					710					715					720
Ser	Arg	Cys	Pro	Thr	Glu	Cys	Thr	Cys	Leu	Asp	Thr	Val	Val	Arg	Cys
				725					730					735	
Ser	Asn	Lys	Gly	Leu	Lys	Val	Leu	Pro	Lys	Gly	Ile	Pro	Arg	Asp	Val
			740					745					750		
Thr	Glu	Leu	Tyr	Leu	Asp	Gly	Asn	Gln	Phe	Thr	Leu	Val	Pro	Lys	Glu
		755					760					765			
Leu	Ser	Asn	Tyr	Lys	His	Leu	Thr	Leu	Ile	Asp	Leu	Ser	Asn	Asn	Arg
		770				775					780				
Ile	Ser	Thr	Leu	Ser	Asn	Gln	Ser	Phe	Ser	Asn	Met	Thr	Gln	Leu	Leu
785					790					795					800
Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	Leu	Arg	Cys	Ile	Pro	Pro	Arg	Thr
				805					810					815	
Phe	Asp	Gly	Leu	Lys	Ser	Leu	Arg	Leu	Leu	Ser	Leu	His	Gly	Asn	Asp
			820					825					830		
Ile	Ser	Val	Val	Pro	Glu	Gly	Ala	Phe	Asn	Asp	Leu	Ser	Ala	Leu	Ser
		835					840					845			
His	Leu	Ala	Ile	Gly	Ala	Asn	Pro	Leu	Tyr	Cys	Asp	Cys	Asn	Met	Gln
		850				855					860				

Trp	Leu	Ser	Asp	Trp	Val	Lys	Ser	Glu	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	
865					870					875					880	
Arg	Cys	Ala	Gly	Pro	Gly	Glu	Met	Ala	Asp	Lys	Leu	Leu	Leu	Thr	Thr	
				885					890					895		
Pro	Ser	Lys	Lys	Phe	Thr	Cys	Gln	Gly	Pro	Val	Asp	Val	Asn	Ile	Leu	
				900					905					910		
Ala	Lys	Cys	Asn	Pro	Cys	Leu	Ser	Asn	Pro	Cys	Lys	Asn	Asp	Gly	Thr	
		915					920					925				
Cys	Asn	Ser	Asp	Pro	Val	Asp	Phe	Tyr	Arg	Cys	Thr	Cys	Pro	Tyr	Gly	
	930					935					940					
Phe	Lys	Gly	Gln	Asp	Cys	Asp	Val	Pro	Ile	His	Ala	Cys	Ile	Ser	Asn	
945					950					955					960	
Pro	Cys	Lys	His	Gly	Gly	Thr	Cys	His	Leu	Lys	Glu	Gly	Glu	Glu	Asp	
				965					970					975		
Gly	Phe	Trp	Cys	Ile	Cys	Ala	Asp	Gly	Phe	Glu	Gly	Glu	Asn	Cys	Glu	
			980					985					990			
Val	Asn	Val	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	Glu	Asn	Asn	Ser	Thr	
		995					1000					1005				
Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Thr	Cys	Leu	Cys	Pro	Pro	Glu	Tyr	
	1010					1015					1020					
Thr	Gly	Glu	Leu	Cys	Glu	Glu	Lys	Leu	Asp	Phe	Cys	Ala	Gln	Asp	Leu	
1025					1030					1035					1040	
Asn	Pro	Cys	Gln	His	Asp	Ser	Lys	Cys	Ile	Leu	Thr	Pro	Lys	Gly	Phe	
				1045					1050					1055		
Lys	Cys	Asp	Cys	Thr	Pro	Gly	Tyr	Val	Gly	Glu	His	Cys	Asp	Ile	Asp	
		1060					1065						1070			
Phe	Asp	Asp	Cys	Gln	Asp	Asn	Lys	Cys	Lys	Asn	Gly	Ala	His	Cys	Thr	
	1075						1080					1085				
Asp	Ala	Val	Asn	Gly	Tyr	Thr	Cys	Ile	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	
	1090					1095					1100					
Leu	Phe	Cys	Glu	Phe	Ser	Pro	Pro	Met	Val	Leu	Pro	Arg	Thr	Ser	Pro	
1105					1110					1115					1120	
Cys	Asp	Asn	Phe	Asp	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Arg	Ile	
			1125					1130					1135			
Asn	Glu	Pro	Ile	Cys	Gln	Cys	Leu	Pro	Gly	Tyr	Gln	Gly	Glu	Lys	Cys	
		1140					1145						1150			
Glu	Lys	Leu	Val	Ser	Val	Asn	Phe	Ile	Asn	Lys	Glu	Ser	Tyr	Leu	Gln	
	1155					1160						1165				
Ile	Pro	Ser	Ala	Lys	Val	Arg	Pro	Gln	Thr	Asn	Ile	Thr	Leu	Gln	Ile	
	1170					1175					1180					
Ala	Thr	Asp	Glu	Asp	Ser	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp	Lys	Asp	
1185					1190					1195				1200		
His	Ile	Ala	Val	Glu	Leu	Tyr	Arg	Gly	Arg	Val	Arg	Ala	Ser	Tyr	Asp	
			1205					1210						1215		

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 Ser Pro Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly
 1 5 10 15
 Leu Met Glu Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg
 20 25 30
 Leu Glu Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln
 35 40 45
 Tyr Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
 50 55 60
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu Val
 65 70 75 80
 Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe Asp Gly
 85 90 95
 Leu Val Ser Leu Gln Leu Leu Leu Leu
 100 105

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 <211> 138
 <212> PRT
 <213> human

<400> 4
 Glu Gly Ala Phe Asn Gly Ala Ala Ser Val Gln Glu Leu Met Leu Thr
 1 5 10 15
 Gly Asn Gln Leu Glu Thr Val His Gly Arg Gly Phe Arg Gly Gly Leu
 20 25 30
 Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn Leu Ile Gly Cys Val
 35 40 45
 Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser Val Arg Leu Leu Ser Leu
 50 55 60
 Tyr Asp Asn Arg Ile Thr Thr Ile Thr Pro Gly Ala Phe Thr Thr Leu
 65 70 75 80
 Val Ser Leu Ser Thr Ile Asn Leu Leu Ser Asn Pro Phe Asn Cys Asn
 85 90 95
 Cys His Leu Gly Ala Gly Leu Gly Lys Trp Leu Arg Lys Arg Arg Ile
 100 105 110
 Val Ser Gly Asn Pro Arg Cys Gln Lys Pro Phe Phe Leu Lys Glu Ile
 115 120 125
 Pro Ile Gln Gly Val Gly His Pro Gly Ile
 130 135

<210> 5
 <211> 160
 <212> PRT
 <213> human

<220>
 <221> misc_feature
 <222> (121)..(150)

<223> note="Xaa signifies gap in sequence"

<400> 5

Trp Pro Arg Cys Glu Cys Met Pro Gly Tyr Ala Gly Asp Asn Cys Ser
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Glu Asn Gln Asp Asp Cys Arg Asp His Arg Cys Gln Asn Gly Ala Gln
20 25 30
Cys Met Asp Glu Val Asn Ser Tyr Ser Cys Leu Cys Ala Glu Gly Tyr
35 40 45
Ser Gly Gln Leu Cys Glu Ile Pro Pro His Leu Pro Ala Pro Lys Ser
50 55 60
Pro Cys Glu Gly Thr Glu Cys Gln Asn Gly Ala Asn Cys Val Asp Gln
65 70 75 80
Gly Asn Arg Pro Val Cys Gln Cys Leu Pro Gly Phe Gly Gly Pro Glu
85 90 95
Cys Glu Lys Leu Leu Ser Val Asn Phe Val Asp Arg Asp Thr Tyr Leu
100 105 110
Gln Phe Thr Asp Leu Gln Asn Trp Xaa Arg Xaa Asn Ile Thr Leu Gln
115 120 125
Val Phe Thr Ala Glu Asp Asn Gly Ile Leu Leu Tyr Asn Gly Gly Asn
130 135 140
Asp His Ile Ala Val Xaa Leu Tyr Xaa Gly His Val Arg Phe Ser Tyr
145 150 155 160

<210> 6

<211> 103

<212> PRT

<213> human

<400> 6

Gln Cys His Ile Ser Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro
1 5 10 15
Gly Phe Ser Gly Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln
20 25 30
Val Val Arg Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala
35 40 45
Thr Ala Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro
50 55 60
Gln Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
65 70 75 80
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu Glu
85 90 95
Cys Gly Cys Leu Ala Cys Ser
100

<210> 7

<211> 1480

Leu	Pro	Pro	Lys 340	Ser	Phe	Ser	Ser	Phe 345	Arg	Arg	Leu	Arg	Arg 350	Ile	Asp
Leu	Ser	Asn 355	Asn	Asn	Ile	Ser	Arg 360	Ile	Ala	His	Asp	Ala 365	Leu	Ser	Gly
Leu	Lys 370	Gln	Leu	Thr	Thr	Leu 375	Val	Leu	Tyr	Gly	Asn 380	Lys	Ile	Lys	Asp
Leu 385	Pro	Ser	Gly	Val	Phe 390	Lys	Gly	Leu	Gly	Ser 395	Leu	Arg	Leu	Leu	Leu 400
Leu	Asn	Ala	Asn	Glu 405	Ile	Ser	Cys	Ile	Arg 410	Lys	Asp	Ala	Phe	Arg 415	Asp
Leu	His	Ser	Leu 420	Ser	Leu	Leu	Ser	Leu 425	Tyr	Asp	Asn	Asn	Ile 430	Gln	Ser
Leu	Ala	Asn 435	Gly	Thr	Phe	Asp	Ala 440	Met	Lys	Ser	Met	Lys 445	Thr	Val	His
Leu	Ala 450	Lys	Asn	Pro	Phe	Ile 455	Cys	Asp	Cys	Asn	Leu 460	Arg	Trp	Leu	Ala
Asp 465	Tyr	Leu	His	Lys	Asn 470	Pro	Ile	Glu	Thr	Ser 475	Gly	Ala	Arg	Cys	Glu 480
Ser	Pro	Lys	Arg	Met 485	His	Arg	Arg	Arg	Ile 490	Glu	Ser	Leu	Arg	Glu 495	Glu
Lys	Phe	Lys	Cys 500	Ser	Trp	Gly	Glu 505	Leu	Arg	Met	Lys	Leu	Ser 510	Gly	Glu
Cys	Arg	Met 515	Asp	Ser	Asp	Cys	Pro 520	Ala	Met	Cys	His	Cys 525	Glu	Gly	Thr
Thr 530	Val	Asp	Cys	Thr	Gly	Arg 535	Arg	Leu	Lys	Glu	Ile 540	Pro	Arg	Asp	Ile
Pro 545	Leu	His	Thr	Thr	Glu 550	Leu	Leu	Leu	Asn	Asp 555	Asn	Glu	Leu	Gly	Arg 560
Ile	Ser	Ser	Asp	Gly 565	Leu	Phe	Gly	Arg	Leu 570	Pro	His	Leu	Val	Lys 575	Leu
Glu	Leu	Lys	Arg 580	Asn	Gln	Leu	Thr	Gly 585	Ile	Glu	Pro	Asn	Ala 590	Phe	Glu
Gly	Ala	Ser 595	His	Ile	Gln	Glu	Leu 600	Gln	Leu	Gly	Glu	Asn 605	Lys	Ile	Lys
Glu	Ile 610	Ser	Asn	Lys	Met	Phe 615	Leu	Gly	Leu	His	Gln 620	Leu	Lys	Thr	Leu
Asn 625	Leu	Tyr	Asp	Asn	Gln 630	Ile	Ser	Cys	Val	Met 635	Pro	Gly	Ser	Phe	Glu 640
His	Leu	Asn	Ser	Leu 645	Thr	Ser	Leu	Asn	Leu 650	Ala	Ser	Asn	Pro	Phe 655	Asn
Cys	Asn	Cys	His 660	Leu	Ala	Trp	Phe	Ala 665	Glu	Cys	Val	Arg	Lys 670	Lys	Ser
Leu	Asn	Gly 675	Gly	Ala	Ala	Arg	Cys 680	Gly	Ala	Pro	Ser	Lys 685	Val	Arg	Asp

Cys Met Asp His Phe Thr His Tyr Ser Cys Asp Cys Gln Ala Gly Phe
 1045 1050 1055
 His Gly Thr Asn Cys Thr Asp Asn Ile Asp Asp Cys Gln Asn His Met
 1060 1065 1070
 Cys Gln Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Asp Tyr Gln Cys
 1075 1080 1085
 Arg Cys Pro Asp Asp Tyr Thr Gly Lys Tyr Cys Glu Gly His Asn Met
 1090 1095 1100
 Ile Ser Met Met Tyr Pro Gln Thr Ser Pro Cys Gln Asn His Glu Cys
 1105 1110 1115 1120
 Lys His Gly Val Cys Phe Gln Pro Asn Ala Gln Gly Ser Asp Tyr Leu
 1125 1130 1135
 Cys Arg Cys His Pro Gly Tyr Thr Gly Lys Trp Cys Glu Tyr Leu Thr
 1140 1145 1150
 Ser Ile Ser Phe Val His Asn Asn Ser Phe Val Glu Leu Glu Pro Leu
 1155 1160 1165
 Arg Thr Arg Pro Glu Ala Asn Val Thr Ile Val Phe Ser Ser Ala Glu
 1170 1175 1180
 Gln Asn Gly Ile Leu Met Tyr Asp Gly Gln Asp Ala His Leu Ala Val
 1185 1190 1195 1200
 Glu Leu Phe Asn Gly Arg Ile Arg Val Ser Tyr Asp Val Gly Asn His
 1205 1210 1215
 Pro Val Ser Thr Met Tyr Ser Phe Glu Met Val Ala Asp Gly Lys Tyr
 1220 1225 1230
 His Ala Val Glu Leu Leu Ala Ile Lys Lys Asn Phe Thr Leu Arg Val
 1235 1240 1245
 Asp Arg Gly Leu Ala Arg Ser Ile Ile Asn Glu Gly Ser Asn Asp Tyr
 1250 1255 1260
 Leu Lys Leu Thr Thr Pro Met Phe Leu Gly Gly Leu Pro Val Asp Pro
 1265 1270 1275 1280
 Ala Gln Gln Ala Tyr Lys Asn Trp Gln Ile Arg Asn Leu Thr Ser Phe
 1285 1290 1295
 Lys Gly Cys Met Lys Glu Val Trp Ile Asn His Lys Leu Val Asp Phe
 1300 1305 1310
 Gly Asn Ala Gln Arg Gln Gln Lys Ile Thr Pro Gly Cys Ala Leu Leu
 1315 1320 1325
 Glu Gly Glu Gln Gln Glu Glu Glu Asp Asp Glu Gln Asp Phe Met Asp
 1330 1335 1340
 Glu Thr Pro His Ile Lys Glu Glu Pro Val Asp Pro Cys Leu Glu Asn
 1345 1350 1355 1360
 Lys Cys Arg Arg Gly Ser Arg Cys Val Pro Asn Ser Asn Ala Arg Asp
 1365 1370 1375
 Gly Tyr Gln Cys Lys Cys Lys His Gly Gln Arg Gly Arg Tyr Cys Asp
 1380 1385 1390

Gln Gly Glu Gly Ser Thr Glu Pro Pro Thr Val Thr Ala Ala Ser Thr
1395 1400 1405

Cys Arg Lys Glu Gln Val Arg Glu Tyr Tyr Thr Glu Asn Asp Cys Arg
1410 1415 1420

Ser Arg Gln Pro Leu Lys Tyr Ala Lys Cys Val Gly Gly Cys Gly Asn
1425 1430 1435 1440

Gln Cys Cys Ala Ala Lys Ile Val Arg Arg Arg Lys Val Arg Met Val
1445 1450 1455

Cys Ser Asn Asn Arg Lys Tyr Ile Lys Asn Leu Asp Ile Val Arg Lys
1460 1465 1470

Cys Gly Cys Thr Lys Lys Cys Tyr
1475 1480

<210> 8
<211> 155
<212> PRT
<213> Caenorhabditis elegans

<220>
<221> misc_feature
<222> (4)..(152)
<223> note="Xaa signifies gap in sequence"

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Arg Asn Pro Xaa Ile Cys Asp Cys Asn Leu Gln Trp Leu Ala Gln Ile
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Asn Leu Gln Lys Asn Ile Glu Thr Ser Gly Ala Arg Cys Glu Gln Pro
20 25 30

Lys Arg Leu Arg Lys Lys Lys Phe Ala Thr Leu Pro Pro Asn Lys Phe
35 40 45

Lys Cys Lys Gly Ser Glu Ser Phe Val Ser Met Tyr Ala Asp Ser Cys
50 55 60

Phe Ile Asp Ser Ile Cys Pro Thr Gln Cys Asp Cys Tyr Gly Thr Thr
65 70 75 80

Val Asp Cys Asn Lys Arg Gly Leu Asn Thr Ile Pro Thr Ser Ile Pro
85 90 95

Arg Phe Ala Thr Gln Leu Leu Leu Ser Gly Asn Asn Ile Ser Thr Val
100 105 110

Asp Leu Asn Ser Asn Ile His Val Leu Glu Asn Leu Glu Xaa Leu Asp
115 120 125

Leu Ser Asn Asn His Ile Thr Phe Ile Asn Asp Lys Ser Phe Glu Lys
130 135 140

Leu Ser Lys Leu Arg Glu Leu Xaa Leu Asn Asp
145 150 155

<210> 9
<211> 735
<212> PRT
<213> Caenorhabditis elegans

<400> 9
 Ser Asn Lys Asn Leu Thr Ser Phe Pro Ser Arg Ile Pro Phe Asp Thr
 1 5 10 15
 Thr Glu Leu Tyr Leu Asp Ala Asn Tyr Ile Asn Glu Ile Pro Ala His
 20 25 30
 Asp Leu Asn Arg Leu Tyr Ser Leu Thr Lys Leu Asp Leu Ser His Asn
 35 40 45
 Arg Leu Ile Ser Leu Glu Asn Asn Thr Phe Ser Asn Leu Thr Arg Leu
 50 55 60
 Ser Thr Leu Ile Ile Ser Tyr Asn Lys Leu Arg Cys Leu Gln Pro Leu
 65 70 75 80
 Ala Phe Asn Gly Leu Asn Ala Leu Arg Ile Leu Ser Leu His Gly Asn
 85 90 95
 Asp Ile Ser Phe Leu Pro Gln Ser Ala Phe Ser Asn Leu Thr Ser Ile
 100 105 110
 Thr His Ile Ala Val Gly Ser Asn Ser Leu Tyr Cys Asp Cys Asn Met
 115 120 125
 Ala Trp Phe Ser Lys Trp Ile Lys Ser Lys Phe Ile Glu Ala Gly Ile
 130 135 140
 Ala Arg Cys Glu Tyr Pro Asn Thr Val Ser Asn Gln Leu Leu Leu Thr
 145 150 155 160
 Ala Gln Pro Tyr Gln Phe Thr Cys Asp Ser Lys Val Pro Thr Lys Leu
 165 170 175
 Ala Thr Lys Cys Asp Leu Cys Leu Asn Ser Pro Cys Lys Asn Asn Ala
 180 185 190
 Ile Cys Glu Thr Thr Ser Ser Arg Lys Tyr Thr Cys Asn Cys Thr Pro
 195 200 205
 Gly Phe Tyr Gly Val His Cys Glu Asn Gln Ile Asp Ala Cys Tyr Gly
 210 215 220
 Ser Pro Cys Leu Asn Asn Ala Thr Cys Lys Val Ala Gln Ala Gly Arg
 225 230 235 240
 Phe Asn Cys Tyr Cys Asn Lys Gly Phe Glu Gly Asp Tyr Cys Glu Lys
 245 250 255
 Asn Ile Asp Asp Cys Val Asn Ser Lys Cys Glu Asn Gly Gly Lys Cys
 260 265 270
 Val Asp Leu Val Arg Phe Cys Ser Glu Glu Leu Lys Asn Phe Gln Ser
 275 280 285
 Phe Gln Ile Asn Ser Tyr Arg Cys Asp Cys Pro Met Glu Tyr Glu Gly
 290 295 300
 Lys His Cys Glu Asp Lys Leu Glu Tyr Cys Thr Lys Lys Leu Asn Pro
 305 310 315 320
 Cys Glu Asn Asn Gly Lys Cys Ile Pro Ile Asn Gly Ser Tyr Ser Cys
 325 330 335
 Met Cys Ser Pro Gly Phe Thr Gly Asn Asn Cys Glu Thr Asn Ile Asp

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340					345					350					
Asp	Cys	Lys	Asn	Val	Glu	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Val	Asp	Gly
		355					360					365			
Ile	Leu	Ser	Tyr	Asp	Cys	Leu	Cys	Arg	Pro	Gly	Tyr	Ala	Gly	Gln	Tyr
	370				375						380				
Cys	Glu	Ile	Pro	Pro	Met	Met	Asp	Met	Glu	Tyr	Gln	Lys	Thr	Asp	Ala
385					390					395					400
Cys	Gln	Gln	Ser	Ala	Cys	Gly	Gln	Gly	Glu	Cys	Val	Ala	Ser	Gln	Asn
				405					410					415	
Ser	Ser	Asp	Phe	Thr	Cys	Lys	Cys	His	Glu	Gly	Phe	Ser	Gly	Pro	Ser
			420					425					430		
Cys	Asp	Arg	Gln	Met	Ser	Val	Gly	Phe	Lys	Asn	Pro	Gly	Ala	Tyr	Leu
		435					440					445			
Ala	Leu	Asp	Pro	Leu	Ala	Ser	Asp	Gly	Thr	Ile	Thr	Met	Thr	Leu	Arg
	450					455					460				
Thr	Thr	Ser	Lys	Ile	Gly	Ile	Leu	Leu	Tyr	Tyr	Gly	Asp	Asp	His	Phe
465					470					475					480
Val	Ser	Ala	Glu	Leu	Tyr	Asp	Gly	Arg	Val	Lys	Leu	Val	Tyr	Tyr	Ile
				485					490					495	
Gly	Asn	Phe	Pro	Ala	Ser	His	Met	Tyr	Ser	Ser	Val	Lys	Val	Asn	Asp
			500					505					510		
Gly	Leu	Pro	His	Arg	Ile	Ser	Ile	Arg	Thr	Ser	Glu	Arg	Lys	Cys	Phe
		515					520					525			
Leu	Gln	Ile	Asp	Lys	Asn	Pro	Val	Gln	Ile	Val	Glu	Asn	Ser	Gly	Lys
	530					535					540				
Ser	Asp	Gln	Leu	Ile	Thr	Lys	Gly	Lys	Glu	Met	Leu	Tyr	Ile	Gly	Gly
545					550					555					560
Leu	Pro	Ile	Glu	Lys	Ser	Gln	Asp	Ala	Lys	Arg	Arg	Phe	His	Val	Lys
				565					570					575	
Asn	Ser	Glu	Ser	Leu	Lys	Gly	Cys	Ile	Ser	Ser	Ile	Thr	Ile	Asn	Glu
			580					585					590		
Val	Pro	Ile	Asn	Leu	Gln	Gln	Ala	Leu	Glu	Asn	Val	Asn	Thr	Glu	Gln
		595					600					605			
Ser	Cys	Ser	Ala	Thr	Val	Asn	Phe	Cys	Ala	Gly	Ile	Asp	Cys	Gly	Asn
	610					615					620				
Gly	Lys	Cys	Thr	Asn	Asn	Ala	Leu	Ser	Pro	Lys	Gly	Tyr	Met	Cys	Gln
625					630					635					640
Cys	Asp	Ser	His	Phe	Ser	Gly	Glu	His	Cys	Asp	Glu	Lys	Arg	Ile	Lys
				645					650					655	
Cys	Asp	Lys	Gln	Lys	Phe	Arg	Arg	His	His	Ile	Glu	Asn	Glu	Cys	Arg
			660					665					670		
Ser	Val	Asp	Arg	Ile	Lys	Ile	Ala	Glu	Cys	Asn	Gly	Tyr	Cys	Gly	Gly
		675					680					685			
Glu	Gln	Asn	Cys	Cys	Thr	Ala	Val	Lys	Lys	Lys	Gln	Arg	Lys	Val	Lys

690 695 700
 Met Ile Cys Lys Asn Gly Thr Thr Lys Ile Ser Thr Val His Ile Ile
 705 710 715 720
 Arg Gln Cys Gln Cys Glu Pro Thr Lys Ser Val Leu Ser Glu Lys
 725 730 735

 <210> 10
 <211> 154

 <212> PRT
 <213> mouse

 <400> 10
 Asp Pro Leu Pro Val His His Arg Cys Glu Cys Met Leu Gly Tyr Thr
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 Gly Asp Asn Cys Ser Glu Asn Gln Asp Asp Cys Lys Asp His Lys Cys
 20 25 30
 Gln Asn Gly Ala Gln Cys Val Asp Glu Val Asn Ser Tyr Ala Cys Leu
 35 40 45
 Cys Val Glu Gly Tyr Ser Gly Gln Leu Cys Glu Ile Pro Pro Ala Pro
 50 55 60
 Arg Ser Ser Cys Glu Gly Thr Glu Cys Gln Asn Gly Ala Asn Cys Val
 65 70 75 80
 Asp Gln Gly Ser Arg Pro Val Cys Gln Cys Leu Pro Gly Phe Gly Gly
 85 90 95
 Pro Glu Cys Glu Lys Leu Leu Ser Val Asn Phe Val Asp Arg Asp Thr
 100 105 110
 Tyr Leu Gln Phe Thr Asp Leu Gln Asn Trp Pro Arg Ala Asn Ile Thr
 115 120 125
 Leu Gln Val Ser Thr Ala Glu Asp Asn Gly Ile Leu Leu Tyr Asn Gly
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 Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val Pro Ile Met Glu
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 Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro Ile Arg Ser Lys
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Arg Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro
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Arg Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp
65 70 75 80
Tyr Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg
85 90 95
Asp Leu Glu Val Leu Thr Leu Asn Asn Asn Ile Thr Arg Leu Ser
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Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe Asn
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Val Gly Gln Pro Tyr Cys Glu Cys Asn Ser Gly Phe Thr Gly Asp Ser
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Cys Ala Ser

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Gln	Val	Thr	Ile 610	Ser	Gly	Leu	Thr 615	Pro	Gly	Thr	Ser	Thr	Val	Phe	Leu 620
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Thr	Thr	Thr	Leu	Val	Leu	Ser	Asn	Gln	Gln	Pro	Ala	Trp	Leu	Asn	Asp		
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Lys	Met	Leu	Arg	Ala	Pro	Ala	Met	Pro	Thr	Asn	Pro	Val	Pro	Pro	Glu		
		1060						1065					1070				
Pro	Pro	Ala	Arg	Tyr	Ala	Asp	His	Thr	Ala	Gly	Arg	Arg	Ser	Arg	Ser		
	1075					1080						1085					
Ser	Arg	Ala	Ser	Asp	Gly	Arg	Gly	Thr	Leu	Asn	Gly	Gly	Leu	His	His		
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Arg	Thr	Ser	Gly	Ser	Gln	Arg	Ser	Asp	Ser	Pro	Pro	His	Thr	Asp	Val		
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Ser	Tyr	Val	Gln	Leu	His	Ser	Ser	Asp	Gly	Thr	Gly	Ser	Ser	Lys	Glu		
			1125						1130					1135			
Arg	Thr	Gly	Glu	Arg	Arg	Thr	Pro	Pro	Asn	Lys	Thr	Leu	Met	Asp	Phe		
		1140						1145					1150				
Ile	Pro	Pro	Pro	Pro	Ser	Asn	Pro	Pro	Pro	Pro	Gly	Gly	His	Val	Tyr		
	1155					1160						1165					
Asp	Thr	Ala	Thr	Arg	Arg	Gln	Leu	Asn	Arg	Gly	Ser	Thr	Pro	Arg	Glu		
	1170					1175					1180						
Asp	Thr	Tyr	Asp	Ser	Val	Ser	Asp	Gly	Ala	Phe	Ala	Arg	Val	Asp	Val		
1185					1190				1195						1200		
Asn	Ala	Arg	Pro	Thr	Ser	Arg	Asn	Arg	Asn	Leu	Gly	Gly	Arg	Pro	Leu		
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Lys	Gly	Lys	Arg	Asp	Asp	Asp	Ser	Gln	Arg	Ser	Ser	Leu	Met	Met	Asp		
		1220						1225					1230				
Asp	Asp	Gly	Gly	Ser	Ser	Glu	Ala	Asp	Gly	Glu	Asn	Ser	Glu	Gly	Asp		
	1235					1240					1245						
Val	Pro	Arg	Gly	Gly	Val	Arg	Lys	Ala	Val	Pro	Arg	Met	Gly	Ile	Ser		
	1250				1255						1260						
Ala	Ser	Thr	Leu	Ala	His	Ser	Cys	Tyr	Gly	Thr	Asn	Gly	Thr	Ala	Gln		
1265					1270					1275					1280		
Arg	Phe	Arg	Ser	Ile	Pro	Arg	Asn	Asn	Gly	Ile	Val	Thr	Gln	Glu	Gln		
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Thr

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 <212> PRT
 <213> human

<400> 18
 Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
 1 5 10 15
 Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu

[illegible]

Pro	Ser	Ala	Pro	Ser	Lys	Pro	Glu	Val	Thr	Asp	Val	Ser	Arg	Asn	Thr
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Val	Thr	Leu	Ser	Trp	Gln	Pro	Asn	Leu	Asn	Ser	Gly	Ala	Thr	Pro	Thr
			580					585					590		
Ser	Tyr	Ile	Ile	Glu	Ala	Phe	Ser	His	Ala	Ser	Gly	Ser	Ser	Trp	Gln
		595					600					605			
Thr	Val	Ala	Glu	Asn	Val	Lys	Thr	Glu	Thr	Ser	Ala	Ile	Lys	Gly	Leu
	610					615					620				
Lys	Pro	Asn	Ala	Ile	Tyr	Leu	Phe	Leu	Val	Arg	Ala	Ala	Asn	Ala	Tyr
625					630					635					640
Gly	Ile	Ser	Asp	Pro	Ser	Gln	Ile	Ser	Asp	Pro	Val	Lys	Thr	Gln	Asp
				645					650					655	
Val	Leu	Pro	Thr	Ser	Gln	Gly	Val	Asp	His	Lys	Gln	Val	Gln	Arg	Glu
			660					665					670		
Leu	Gly	Asn	Ala	Val	Leu	His	Leu	His	Asn	Pro	Thr	Val	Val	Leu	Ser
		675					680					685			Ser
Ser	Ser	Ile	Glu	Val	His	Trp	Thr	Val	Asp	Gln	Gln	Ser	Gln	Tyr	Ile
		690				695					700				
Gln	Gly	Tyr	Lys	Ile	Leu	Tyr	Arg	Pro	Ser	Gly	Ala	Asn	His	Gly	Glu
705					710					715					720
Ser	Asp	Trp	Leu	Val	Phe	Glu	Val	Arg	Thr	Pro	Ala	Lys	Asn	Ser	Val
				725					730					735	
Val	Ile	Pro	Asp	Leu	Arg	Lys	Gly	Val	Asn	Tyr	Glu	Ile	Lys	Ala	Arg
			740					745					750		
Pro	Phe	Phe	Asn	Glu	Phe	Gln	Gly	Ala	Asp	Ser	Glu	Ile	Lys	Phe	Ala
		755					760					765			
Lys	Thr	Leu	Glu	Glu	Ala	Pro	Ser	Ala	Pro	Pro	Gln	Gly	Val	Thr	Val
	770					775					780				
Ser	Lys	Asn	Asp	Gly	Asn	Gly	Thr	Ala	Ile	Leu	Val	Ser	Trp	Gln	Pro
785					790					795					800
Pro	Pro	Glu	Asp	Thr	Gln	Asn	Gly	Met	Val	Gln	Glu	Tyr	Lys	Val	Trp
				805					810					815	
Cys	Leu	Gly	Asn	Glu	Thr	Arg	Tyr	His	Ile	Asn	Lys	Thr	Val	Asp	Gly
			820					825					830		
Ser	Thr	Phe	Ser	Val	Val	Ile	Pro	Phe	Leu	Val	Pro	Gly	Ile	Arg	Tyr
		835					840					845			
Ser	Val	Glu	Val	Ala	Ala	Ser	Thr	Gly	Ala	Gly	Ser	Gly	Val	Lys	Ser
		850				855					860				
Glu	Pro	Gln	Phe	Ile	Gln	Leu	Asp	Ala	His	Gly	Asn	Pro	Val	Ser	Pro
865					870					875					880
Glu	Asp	Gln	Val	Ser	Leu	Ala	Gln	Gln	Ile	Ser	Asp	Val	Val	Lys	Gln
				885					890					895	
Pro	Ala	Phe	Ile	Ala	Gly	Ile	Gly	Ala	Ala	Cys	Trp	Ile	Ile	Leu	Met
			900					905					910		
Val	Phe	Ser	Ile	Trp	Leu	Tyr	Arg	His	Arg	Lys	Lys	Arg	Asn	Gly	Leu
		915					920					925			
Thr	Ser	Thr	Tyr	Ala	Gly	Ile	Arg	Lys	Val	Pro	Ser	Phe	Thr	Phe	Thr
		930				935					940				
Pro	Thr	Val	Thr	Tyr	Gln	Arg	Gly	Gly	Glu	Ala	Val	Ser	Ser	Gly	Gly
945					950					955					960
Arg	Pro	Gly	Leu	Leu	Asn	Ile	Ser	Glu	Pro	Ala	Ala	Gln	Pro	Trp	Leu
				965					970					975	
Ala	Asp	Thr	Trp	Pro	Asn	Thr	Gly	Asn	Asn	His	Asn	Asp	Cys	Ser	Ile
			980					985					990		
Ser	Cys	Cys	Thr	Ala	Gly	Asn	Gly	Asn	Ser	Asp	Ser	Asn	Leu	Thr	Thr
		995					1000					1005			
Tyr	Ser	Arg	Pro	Ala	Asp	Cys	Ile	Ala	Asn	Tyr	Asn	Asn	Gln	Leu	Asp
		1010				1015					1020				
Asn	Lys	Gln	Thr	Asn	Leu	Met	Leu	Pro	Glu	Ser	Thr	Val	Tyr	Gly	Asp
1025					1030					1035					1040
Val	Asp	Leu	Ser	Asn	Lys	Ile	Asn	Glu	Met	Lys	Thr	Phe	Asn	Ser	Pro
				1045					1050					1055	
Asn	Leu	Lys	Asp	Gly	Arg	Phe	Val	Asn	Pro	Ser	Gly	Gln	Pro	Thr	Pro
			1060					1065					1070		
Tyr	Ala	Thr	Thr	Gln	Leu	Ile	Gln	Ser	Asn	Leu	Ser	Asn	Asn	Met	Asn
		1075					1080						1085		
Asn	Gly	Ser	Gly	Asp	Ser	Gly	Glu	Lys	His	Trp	Lys	Pro	Leu	Gly	Gln

1090	Gln Lys Gln Glu Val	1095	Ala Pro Val Gln Tyr	1100	Asn Ile Val Glu Gln Asn
1105	Lys Leu Asn Lys Asp	1110	Tyr Arg Ala Asn Asp	1115	Thr Val Pro Pro Thr Ile
	1125		1130		1135
Pro Tyr Asn Gln Ser	Tyr Asp Gln Asn	Thr Gly Gly Ser	Tyr Asn Ser		
	1140		1145		1150
Ser Asp Arg Gly Ser	Ser Thr Ser Gly	Ser Gln Gly His	Lys Lys Gly		
	1155		1160		1165
Ala Arg Thr Pro Lys	Val Pro Lys Gln	Gly Gly Met Asn	Trp Ala Asp		
	1170		1175		1180
Leu Leu Pro Pro Pro	Pro Ala His Pro	Pro Pro Pro His	Ser Asn Ser Glu		
1185		1190		1195	1200
Glu Tyr Asn Ile Ser	Val Asp Glu Ser	Tyr Asp Gln Glu	Met Pro Cys		
	1205		1210		1215
Pro Val Pro Pro Ala	Arg Met Tyr Leu	Gln Gln Asp Glu	Leu Glu Glu		
	1220		1225		1230
Glu Glu Asp Glu Arg	Gly Pro Thr Pro	Pro Val Arg Gly	Ala Ala Ser		
	1235		1240		1245
Ser Pro Ala Ala Val	Ser Tyr Ser His	Gln Ser Thr Ala	Thr Leu Thr		
	1250		1255		1260
Pro Ser Pro Gln Glu	Glu Leu Gln Pro	Met Leu Gln Asp	Cys Pro Glu		
1265		1270		1275	1280
Glu Thr Gly His Met	Gln His Gln Pro	Asp Arg Arg Arg	Gln Pro Val		
	1285		1290		1295
Ser Pro Pro Pro Pro	Pro Arg Pro Ile	Ser Pro Pro His	Thr Tyr Gly		
	1300		1305		1310
Tyr Ile Ser Gly Pro	Leu Val Ser Asp	Met Asp Thr Asp	Ala Pro Glu		
	1315		1320		1325
Glu Glu Glu Asp Glu	Ala Asp Met Glu	Val Ala Lys Met	Gln Thr Arg		
	1330		1335		1340
Arg Leu Leu Leu Arg	Gly Leu Glu Gln	Thr Pro Ala Ser	Ser Val Gly		
1345		1350		1355	1360
Asp Leu Glu Ser Ser	Val Thr Gly Ser	Met Ile Asn Gly	Trp Gly Ser		
	1365		1370		1375
Ala Ser Glu Glu Asp	Asn Ile Ser Ser	Gly Arg Ser Ser	Val Ser Ser		
	1380		1385		1390
Ser Asp Gly Ser Phe	Phe Thr Asp Ala	Asp Phe Ala Gln	Ala Val Ala		
	1395		1400		1405
Ala Ala Ala Glu Tyr	Ala Gly Leu Lys	Val Ala Arg Arg	Gln Met Gln		
	1410		1415		1420
Asp Ala Ala Gly Arg	Arg His Phe His	Ala Ser Gln Cys	Pro Arg Pro		
1425		1430		1435	1440
Thr Ser Pro Val Ser	Thr Asp Ser Asn	Met Ser Ala Ala	Val Met Gln		
	1445		1450		1455
Lys Thr Arg Pro Ala	Lys Lys Leu Lys	His Gln Pro Gly	His Leu Arg		
	1460		1465		1470
Arg Glu Thr Tyr Thr	Asp Asp Leu Pro	Pro Pro Pro Val	Pro Pro Pro		
	1475		1480		1485
Ala Ile Lys Ser Pro	Thr Ala Gln Ser	Lys Thr Gln Leu	Glu Val Arg		
	1490		1495		1500
Pro Val Val Val Pro	Lys Leu Pro Ser	Met Asp Ala Arg	Thr Asp Arg		
1505		1510		1515	1520
Ser Ser Asp Arg Lys	Gly Ser Ser Tyr	Lys Gly Arg Glu	Val Leu Asp		
	1525		1530		1535
Gly Arg Gln Val Val	Asp Met Arg Thr	Asn Pro Gly Asp	Pro Arg Glu		
	1540		1545		1550
Ala Gln Glu Gln Gln	Asn Asp Gly Lys	Gly Arg Gly Asn	Lys Ala Ala		
	1555		1560		1565
Lys Arg Asp Leu Pro	Pro Ala Lys Thr	His Leu Ile Gln	Glu Asp Ile		
	1570		1575		1580
Leu Pro Tyr Cys Arg	Pro Thr Phe Pro	Thr Ser Asn Asn	Pro Arg Asp		
1585		1590		1595	1600
Pro Ser Ser Ser Ser	Ser Met Ser Ser	Arg Gly Ser Gly	Ser Arg Gln		
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Arg Glu Gln Ala Asn	Val Gly Arg Arg	Asn Ile Ala Glu	Met Gln Val		
	1620		1625		1630

385					390					395					400
Gln	Arg	Pro	Arg	Pro	Thr	Ser	Pro	Phe	Ser	Thr	Asp	Ser	Asn	Thr	Ser
				405					410					415	
Ala	Ala	Leu	Ser	Gln	Ser	Gln	Arg	Pro	Arg	Pro	Thr	Lys	Lys	His	Lys
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Gly	Gly														

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			20					25					30		
Gln	Cys	Pro	Arg	Pro	Thr	Ser	Pro	Val	Ser	Thr	Asp	Ser	Asn	Met	Ser
		35					40					45			
Ala	Val	Val	Ile	Gln	Lys	Ala	Arg	Pro	Ala	Lys	Lys	Gln	Lys	His	Gln
	50				55						60				
Pro	Gly	His	Leu	Arg	Arg	Glu	Ala	Tyr	Ala	Asp	Asp	Leu	Pro	Pro	Pro
65					70					75				80	
Pro	Val	Pro	Pro	Pro	Ala	Ile	Lys	Ser	Pro	Thr	Val	Gln	Ser	Lys	Ala
				85					90					95	
Gln	Leu	Glu	Val	Arg	Pro	Val	Met	Val	Pro	Lys	Leu	Ala	Ser	Ile	Glu
			100				105						110		
Ala	Arg	Thr	Asp	Arg	Ser	Ser	Asp	Arg	Lys	Gly	Gly	Ser	Tyr	Lys	Gly
		115					120					125			
Arg	Glu	Ala	Leu	Asp	Gly	Arg	Gln	Val	Thr	Asp	Leu	Arg	Thr	Asn	Pro
	130					135					140				
Ser	Asp	Pro	Arg												
145															